RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _/0/552,013_
Source: _Py/10_
Date Processed by STIC: _/0/18/05_

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RAW SEQUENCE LISTING   DATE: 10/18/2005
PATENT APPLICATION: US/10/552,013   TIME: 10:16:52

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF4\10182005\J552013.raw**

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  3 <110> APPLICANT: Renz, Andreas
  4         Sozer, Nursen
  5         Frentzen, Margit
  6         Bauer, Jorg
  7         Keith, Stobart
  8         Fraser, Thomas
  9         Lazarus, Colin M
 10         Qi, Baoxiu
 11         Abbadi, Amine
 12         Heinz, Ernst
 14 <120> TITLE OF INVENTION: NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED,
MULTIPLY
 15         UNSATURATED FATTY ACIDS
 17 <130> FILE REFERENCE: 13478-00002-US
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/552,013
C--> 19 <141> CURRENT FILING DATE: 2005-09-30
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/003224
 20 <151> PRIOR FILING DATE: 2004-03-26
 22 <150> PRIOR APPLICATION NUMBER: DE103 14 759.4
 23 <151> PRIOR FILING DATE: 2003-03-31
 25 <150> PRIOR APPLICATION NUMBER: DE103 48 996.7
 26 <151> PRIOR FILING DATE: 2003-10-17
 28 <160> NUMBER OF SEQ ID NOS: 122
 30 <170> SOFTWARE: PatentIn version 3.3
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1047
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Thraustochytrium
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (38)..(952)
 40 <223> OTHER INFORMATION: LPAAT
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 46                                             1               5
 47 gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg       103
 48 Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
 49             10              15                  20
 50 ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc       151
 51 Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
 52             25              30                  35
 53 acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc       199
 54 Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys
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55      40                      45                      50
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57 Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
58 55                      60                      65                      70
59 tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg      295
60 Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
61                      75                      80                      85
62 aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac      343
63 Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
64                      90                      95                      100
65 tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc      391
66 Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
67         105                      110                      115
68 ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc      439
69 Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
70      120                      125                      130
71 ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct      487
72 Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
73 135                      140                      145                      150
74 cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg      535
75 Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
76                      155                      160                      165
77 ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag      583
78 Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
79                      170                      175                      180
80 acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag      631
81 Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
82         185                      190                      195
83 ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg      679
84 Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
85      200                      205                      210
86 gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac      727
87 Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
88 215                      220                      225                      230
89 cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag      775
90 Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
91                      235                      240                      245
92 aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg      823
93 Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
94                      250                      255                      260
95 cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc      871
96 Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
97         265                      270                      275
98 gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga      919
99 Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
100      280                      285                      290
101 gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca      972
102 Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
103 295                      300                      305
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104 agcggtccag caacgggaga ttaaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa    1032
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111 <212> TYPE: PRT
113 <213> ORGANISM: Thraustochytrium
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118 1               5                   10                  15
119 Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
120             20                  25                  30
121 Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
122         35                  40                  45
123 Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
124     50                  55                  60
125 Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
126 65                  70                  75                  80
127 Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
128             85                  90                  95
129 Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
130         100                 105                 110
131 Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
132         115                 120                 125
133 Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
134     130                 135                 140
135 Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
136 145                 150                 155                 160
137 Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
138             165                 170                 175
139 Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
140         180                 185                 190
141 Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
142         195                 200                 205
143 Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
144     210                 215                 220
145 Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
146 225                 230                 235                 240
147 Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
148             245                 250                 255
149 Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
150         260                 265                 270
151 Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
152         275                 280                 285
153 Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
154     290                 295                 300
155 Leu
156 305
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 1701
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162 <212> TYPE: DNA
164 <213> ORGANISM: Physcomitrella patens
166 <220> FEATURE:
167 <221> NAME/KEY: misc_feature
168 <223> OTHER INFORMATION: LPAAT
170 <400> SEQUENCE: 3
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173 aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgtttaggt atattctgtc     120
174 aactgaaaac ttgtttaat ttttcttaa attgaaattc tgtgcctgaa agccaactct       180
175 aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct     240
176 tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg     300
177 cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag     360
178 ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt    420
179 gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat     480
180 tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc     540
181 cttgtttggt tgggcatttt acgtttttga gtttctgatg ctgcatagaa agtgggaagt     600
182 ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg     660
183 gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtaccc atccatggct     720
184 ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca     780
185 agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta     840
186 aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga     900
187 gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact     960
188 tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag    1020
189 aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt    1080
190 cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg    1140
191 ctgtatgatc tattttatca aaaggaccag atgttggcca gtttagtaa gacaggctct     1200
192 ttccctgaca gtggaattga agagagccct ttgaacatag tggaaggtgt ttgcaatgtt    1260
193 gctctacacg tagtccttag cggttgggta ttctggtgct tgtttcattc ggtttggttg    1320
194 aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga    1380
195 cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt    1440
196 agttgtaatt ggtttgttta ttccgattcc aaagctgagt ttaagggtga ggctcctctt    1500
197 taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta    1560
198 atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt    1620
199 ctcctttacc catcttgacc agatgccaaa ctcgcaataa agcagatcaa taggtcgtgc    1680
200 cccaaaaaaa aaaaaaaaaa a                                              1701
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205 <211> LENGTH: 714
206 <212> TYPE: DNA
208 <213> ORGANISM: Physcomitrella patens
210 <220> FEATURE:
211 <221> NAME/KEY: CDS
212 <222> LOCATION: (1)..(714)
213 <223> OTHER INFORMATION: LPAAT
215 <400> SEQUENCE: 4
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219   1               5                  10                  15
220 tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc       96
221 Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
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222              20              25              30
223 aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat    144
224 Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
225         35              40              45
226 gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa    192
227 Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
228         50              55              60
229 ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt    240
230 Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
231 65              70              75              80
232 gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac    288
233 Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
234             85              90              95
235 ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta    336
236 Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
237             100             105             110
238 ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca    384
239 Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
240             115             120             125
241 att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat    432
242 Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
243         130             135             140
244 gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca    480
245 Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
246 145             150             155             160
247 ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg    528
248 Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
249             165             170             175
250 gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta    576
251 Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
252             180             185             190
253 ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc    624
254 Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
255         195             200             205
256 gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa    672
257 Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
258         210             215             220
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261 225             230             235
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265 <211> LENGTH: 237
267 <212> TYPE: PRT
269 <213> ORGANISM: Physcomitrella patens
271 <400> SEQUENCE: 5
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275 1               5               10              15
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277         20              25              30
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L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date